SEQUENCE LISTING

	Narva, Kenneth Merlo, Donald						
<120>	Polynucleotides,	Pesticidal	Proteins,	and Novel	Methods	of Usir	ng Them
<130>	MA-708CDC1						
<150> <151>	US 09/850,351 2001-05-07			,			
	US 09/073,898 1998-05-06				•		
<150> <151>	US 08/690,780 1997-10-30						
<150> <151>	US 60/029,848 1996-10-30						
<160>	27 .	•					
<170>	PatentIn version	3.1					,
<210>	1						
<211>	29						
<212>	DNA				•		
<213>	Artificial Seque	nce		•			
			•		·.		
<220>							
<223>	339 forward prim	er	•	•.			
<400>	1			,			
garccr	tgga aagcaaataa t	aaraatgc					29
				•			
<210>	2			ı			
<211>	33			•			
<212>	DNA	٧.					
<213>	Artificial Seque	nce					
<220>			•				
<223>	339 reverse prim	er					
<400>	2		•				
aaartt	atct ccccawgctt c	atctccatt t	tg				33
-210-	3						
<210> <211>							
<211>							
<213>		iensis					
		, -					
<400>	3 aaga ataatactaa a	ttaaggaga a	agaggett ag	caactttta	t toattat	+++	60
acgaac	aaya aladladlad d		gageettae	caageeeea	o oguccac		

T:\Sequences\Mycogen\MA-708CDC1\MA-708CDC1.ST25.txt/DNB/ehm

T:\Sequences\Mycogen\MA-708CDC1\MA-708CDC1.ST25.txt/DNB/ehm

gttaaaggaa	aaccttctat	tcatttaata	gatgaaaata	ctggatatat	tcattatgaa	1860
gatacaaata	ataatttaga	agattatcaa	actattaata	aacgttttac	tacaggaact	1920
gatttaaagg	gagtgtattt	aattttaaaa	agtcaaaatg	gagatgaagc	ttggggagat	1980
aactttatta	ttttggaaat	tagtccttct	gaaaagttat	taagtccaga	attaattaat	2040
acaaataatt	ggacgagtac	gggatcaact	aatattagcg	gtaatacact	cactctttat	2100
cagggaggac	gagggattct	aaaacaaaac	cttcaattag	atagtttttc	aacttataga ,	2160
gtgtatttt	ctgtgtccgg	agatgctaat	gtaaggatta	gaaattctag	ggaagtgtta	2220
tttgaaaaaa	gatatatgag	cggtgctaaa	gatgtttctg	aaatgttcac	tacaaaattt	2280
gagaaagata	acttttatat	agagctttct	caagggaata	atttatatgg	tggtcctatt	2340
gtacattttt	acgatgtctc	tattaagtaa	cccaa		·	2375

<210> 4

<211> 790

<212> PRT

<213> Bacillus thuringiensis

<400> 4

Met Asn Lys Asn Asn Thr Lys Leu Ser Thr Arg Ala Leu Pro Ser Phe 1 5 10 15

Ile Asp Tyr Phe Asn Gly Ile Tyr Gly Phe Ala Thr Gly Ile Lys Asp 20 25 30

Ile Met Asn Met Ile Phe Lys Thr Asp Thr Gly Gly Asp Leu Thr Leu 35 40 45

Asp Glu Ile Leu Lys Asn Gln Gln Leu Leu Asn Asp Ile Ser Gly Lys 50 55 60

Leu Asp Gly Val Asn Gly Ser Leu Asn Asp Leu Ile Ala Gln Gly Asn 65 70 75 80

Leu Asn Thr Glu Leu Ser Lys Glu Ile Leu Lys Ile Ala Asn Glu Gln 85 90 95

Asn Gln Val Leu Asn Asp Val Asn Asn Lys Leu Asp Ala Ile Asn Thr 100 105 110 Met Leu Arg Val Tyr Leu Pro Lys Ile Thr Ser Met Leu Ser Asp Val 115 120 125

Met Lys Gln Asn Tyr Ala Leu Ser Leu Gln Ile Glu Tyr Leu Ser Lys 130 135 . 140

Gln Leu Gln Glu Ile Ser Asp Lys Leu Asp Ile Ile Asn Val Asn Val 145 150 155 160

Leu Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln Arg Ile 165 170 175

Lys Tyr Val Asn Glu Lys Phe Glu Glu Leu Thr Phe Ala Thr Glu Thr 180 185 190

Ser Ser Lys Val Lys Lys Asp Gly Ser Pro Ala Asn Ile Leu Asp Glu 195 200 205

Leu Thr Glu Leu Thr Glu Leu Ala Lys Ser Val Thr Lys Asn Asp Val 210 215 220

Asp Gly Phe Glu Phe Tyr Leu Asn Thr Phe His Asp Val Met Val Gly 225 230 235 240

Asn Asn Leu Phe Gly Arg Ser Ala Leu Lys Thr Ala Ser Glu Leu Ile 245 250 255

Thr Lys Glu Asn Val Lys Thr Ser Gly Ser Glu Val Gly Asn Val Tyr
260 265 270

Asn Phe Leu Ile Val Leu Thr Ala Leu Gln Ala Lys Ala Phe Leu Thr 275 280 285

Leu Thr Thr Cys Arg Lys Leu Leu Gly Leu Ala Asp Ile Asp Tyr Thr 290 295 300

Ser Ile Met Asn Glu His Leu Asn Lys Glu Lys Glu Glu Phe Arg Val 305 310 315 320

Asn Ile Leu Pro Thr Leu Ser Asn Thr Phe Ser Asn Pro Asn Tyr Ala 325 330 335

- Lys Val Lys Gly Ser Asp Glu Asp Ala Lys Met Ile Val Glu Ala Lys 340 345 350
- Pro Gly His Ala Leu Ile Gly Phe Glu Ile Ser Asn Asp Ser Ile Thr 355 360 365
- Val Leu Lys Val Tyr Glu Ala Lys Leu Lys Gln Asn Tyr Gln Val Asp 370 375 380
- Lys Asp Ser Leu Ser Glu Val Ile Tyr Gly Asp Met Asp Lys Leu Leu 385 390 395 400
- Cys Pro Asp Gln Ser Glu Gln Ile Tyr Tyr Thr Asn Asn Ile Val Phe 405 410 415
- Pro Asn Glu Tyr Val Ile Thr Lys Ile Asp Phe Thr Lys Lys Met Lys
 420 425 430
- Thr Leu Arg Tyr Glu Val Thr Ala Asn Phe Tyr Asp Ser Ser Thr Gly
 435 440 445
- Glu Ile Asp Leu Asn Lys Lys Lys Val Glu Ser Ser Glu Ala Glu Tyr 450 455 460
- Lys Thr Leu Ser Ala Asn Asp Asp Gly Val Tyr Met Pro Leu Gly Val 465 470 475 480
- Ile Ser Glu Thr Phe Leu Thr Pro Ile Asn Gly Phe Gly Leu Gln Ala 485 490 495
- Asp Glu Asn Ser Arg Leu Ile Thr Leu Thr Cys Lys Ser Tyr Leu Arg 500 505 510
- Glu Leu Leu Ala Thr Asp Leu Ser Asn Lys Glu Thr Lys Leu Ile 515 520 525
- Val Pro Pro Ser Gly Phe Ile Ser Asn Ile Val Glu Asn Gly Ser Ile 530 535 540
- Glu Glu Asp Asn Leu Glu Pro Trp Lys Ala Asn Asn Lys Asn Ala Tyr 545 550 555 560

Lys Asp Gly Gly Ile Ser Gln Phe Ile Gly Asp Asn Leu Lys Pro Lys 580 585 590

Thr Glu Tyr Val Ile Gln Tyr Thr Val Lys Gly Lys Pro Ser Ile His 595 600 605

Leu Ile Asp Glu Asn Thr Gly Tyr Ile His Tyr Glu Asp Thr Asn Asn 610 620

Asn Leu Glu Asp Tyr Gln Thr Ile Asn Lys Arg Phe Thr Thr Gly Thr 625 630 635 640

Asp Leu Lys Gly Val Tyr Leu Ile Leu Lys Ser Gln Asn Gly Asp Glu 645 650 655

Ala Trp Gly Asp Asn Phe Ile Ile Leu Glu Ile Ser Pro Ser Glu Lys 660 665 670

Leu Leu Ser Pro Glu Leu Ile Asn Thr Asn Asn Trp Thr Ser Thr Gly 675 680 685

Ser Thr Asn Ile Ser Gly Asn Thr Leu Thr Leu Tyr Gln Gly Gly Arg
690 700

Gly Ile Leu Lys Gln Asn Leu Gln Leu Asp Ser Phe Ser Thr Tyr Arg 705 710 715 720

Val Tyr Phe Ser Val Ser Gly Asp Ala Asn Val Arg Ile Arg Asn Ser 725 730 735

Arg Glu Val Leu Phe Glu Lys Arg Tyr Met Ser Gly Ala Lys Asp Val 740 745 750

Ser Glu Met Phe Thr Thr Lys Phe Glu Lys Asp Asn Phe Tyr Ile Glu 755 760 765

Leu Ser Gln Gly Asn Asn Leu Tyr Gly Gly Pro Ile Val His Phe Tyr
770 775 780

Asp Val Ser Ile Lys Pro 785 790

<210> 5 <211> 2370

<212> DNA

<213> Bacillus thuringiensis

<400> 5

atgaacaaga ataatactaa attaagcaca agagccttac caagttttat tgattatttt 60 aatggcattt atggatttgc cactggtatc aaagacatta tgaacatgat ttttaaaacg 120 gatacaggtg gtgatctaac cctagacgaa attttaaaga atcagcagtt actaaatgat 180 atttctggta aattggatgg ggtgaatgga agcttaaatg atcttatcgc acagggaaac 240 ttaaatacag aattatctaa agaaatatta aaaattgcaa atgaacaaaa tcaagtttta 300 aatgatgttg ataacaaact cgatgcgata aatacgatgc ttcgggtata tctacctaaa 360 420 attacctcta tgttgagtga tgtaatgaaa caaaattatg cgctaagtct gcaaatagaa tacttaagta aacaattgca agagatttct gataagttgg atattattaa tgtaaatgta 480 cttattaact ctacacttac tgaaattaca cctgcgtatc aaaggattaa atatgtgaac 540 gaaaaatttg aggaattaac ttttgctaca gaaactagtt caaaagtaaa aaaggatggc 600 teteetgeag atattettga tgagttaaet gagttaaetg aactagegaa aagtgtaaea 660 aaaaatgatg tggatggttt tgaattttac cttaatacat tccacgatgt aatggtagga 720 aataatttat tegggegtte agetttaaaa aetgeategg aattaattae taaagaaaat 780 gtgaaaacaa gtggcagtga ggtcggaaat gtttataact tcttaattgt attaacagct 840 900 ctgcaagcaa aagcttttct tactttaaca acatgccgaa aattattagg cttagcagat 960 attgattata cttctattat gaatgaacat ttaaataagg aaaaagagga atttagagta aacatcctcc ctacactttc taatactttt tctaatccta attatgcaaa agttaaagga 1020 1080 agtgatgaag atgcaaagat gattgtggaa gctaaaccag gacatgcatt ggttgggttt 1140 gaaattagta atgattcaat tacagtatta aaagtatatg aggctaagct aaaacaaaat tatcaagttg ataaggattc cttatcggaa gttatttatg gtgatatgga taaattattg 1200 1260 tgcccagatc aatctgaaca aatctattat acaaataaca tagtatttcc aaatgaatat 1320 gtaattacta aaattgattt tactaaaaaa atgaaaactt taagatatga ggtaacagcg 1380 aatttttatg attcttctac aggagaaatt gacttaaata agaaaaaagt agaatcaagt 1440 gaagcggagt atagaacgtt aagtgctaat gatgatggag tgtatatgcc gttaggtgtc

T:\Sequences\Mycogen\MA-708CDC1\MA-708CDC1.ST25.txt/DNB/ehm

<210> 6

<211> 789

<212> PRT

<213> Bacillus thuringiensis

<400> 6

Met Asn Lys Asn Asn Thr Lys Leu Ser Thr Arg Ala Leu Pro Ser Phe
1 5 10 15

Ile Asp Tyr Phe Asn Gly Ile Tyr Gly Phe Ala Thr Gly Ile Lys Asp 20 25 30

Ile Met Asn Met Ile Phe Lys Thr Asp Thr Gly Gly Asp Leu Thr Leu 35 40 45

Asp Glu Ile Leu Lys Asn Gln Gln Leu Leu Asn Asp Ile Ser Gly Lys 50 55 60 Leu Asp Gly Val Asn Gly Ser Leu Asn Asp Leu Ile Ala Gln Gly Asn 65 70 75 80

Leu Asn Thr Glu Leu Ser Lys Glu Ile Leu Lys Ile Ala Asn Glu Gln 85 90 95

Asn Gln Val Leu Asn Asp Val Asp Asn Lys Leu Asp Ala Ile Asn Thr 100 105 110

Met Leu Arg Val Tyr Leu Pro Lys Ile Thr Ser Met Leu Ser Asp Val 115 120 125

Met Lys Gln Asn Tyr Ala Leu Ser Leu Gln Ile Glu Tyr Leu Ser Lys 130 135 140

Gln Leu Gln Glu Ile Ser Asp Lys Leu Asp Ile Ile Asn Val Asn Val 145 150 155 160

Leu Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln Arg Ile
165 170 175

Lys Tyr Val Asn Glu Lys Phe Glu Glu Leu Thr Phe Ala Thr Glu Thr 180 185 190

Ser Ser Lys Val Lys Lys Asp Gly Ser Pro Ala Asp Ile Leu Asp Glu 195 200 205

Leu Thr Glu Leu Thr Glu Leu Ala Lys Ser Val Thr Lys Asn Asp Val 210 215 220

Asp Gly Phe Glu Phe Tyr Leu Asn Thr Phe His Asp Val Met Val Gly 225 230 235

Asn Asn Leu Phe Gly Arg Ser Ala Leu Lys Thr Ala Ser Glu Leu Ile 245 250 255

Thr Lys Glu Asn Val Lys Thr Ser Gly Ser Glu Val Gly Asn Val Tyr 260 265 270

Asn Phe Leu Ile Val Leu Thr Ala Leu Gln Ala Lys Ala Phe Leu Thr 275 280 285 Leu Thr Thr Cys Arg Lys Leu Leu Gly Leu Ala Asp Ile Asp Tyr Thr 290 295 300

Ser Ile Met Asn Glu His Leu Asn Lys Glu Lys Glu Glu Phe Arg Val 305 310 315. 320

Asn Ile Leu Pro Thr Leu Ser Asn Thr Phe Ser Asn Pro Asn Tyr Ala 325 330 335

Lys Val Lys Gly Ser Asp Glu Asp Ala Lys Met Ile Val Glu Ala Lys 340 345 350

Pro Gly His Ala Leu Val Gly Phe Glu Ile Ser Asn Asp Ser Ile Thr 355 360 365

Val Leu Lys Val Tyr Glu Ala Lys Leu Lys Gln Asn Tyr Gln Val Asp 370 375 380

Lys Asp Ser Leu Ser Glu Val Ile Tyr Gly Asp Met Asp Lys Leu Leu 385 390 395 400

Cys Pro Asp Gln Ser Glu Gln Ile Tyr Tyr Thr Asn Asn Ile Val Phe 405 410 415

Pro Asn Glu Tyr Val Ile Thr Lys Ile Asp Phe Thr Lys Lys Met Lys
420 425 430

Thr Leu Arg Tyr Glu Val Thr Ala Asn Phe Tyr Asp Ser Ser Thr Gly
435 440 445

Glu Ile Asp Leu Asn Lys Lys Lys Val Glu Ser Ser Glu Ala Glu Tyr 450 455 460

Arg Thr Leu Ser Ala Asn Asp Asp Gly Val Tyr Met Pro Leu Gly Val 465 470 475 480

Ile Ser Glu Thr Phe Leu Thr Pro Ile Asn Gly Phe Gly Leu Gln Ala 485 490 495

Asp Glu Asn Ser Arg Leu Ile Thr Leu Thr Cys Lys Ser Tyr Leu Arg 500 505 510

- Glu Leu Leu Ala Thr Asp Leu Ser Asn Lys Glu Thr Lys Leu Ile 515 520 525
- Val Pro Pro Ser Gly Phe Ile Lys Asn Ile Val Glu Asn Gly Ser Ile 530 535 540
- Glu Glu Asp Asn Leu Glu Pro Trp Lys Ala Asn Asn Lys Asn Glu Tyr 545 550 555 560
- Val Asp His Thr Gly Gly Val Asn Gly Thr Lys Ala Leu Tyr Val His 565 570 575
- Lys Asp Gly Gly Ile Ser Gln Phe Ile Gly Asp Lys Leu Lys Pro Lys 580 585 590
- Thr Glu Tyr Val Ile Gln Tyr Thr Val Lys Gly Lys Pro Ser Ile His 595 600 605
- Leu Lys Asp Glu Asn Thr Gly Tyr Ile His Tyr Glu Asp Thr Asn Asn 610 615 620
- Asn Leu Glu Asp Tyr Gln Thr Ile Thr Lys Arg Phe Thr Thr Gly Thr 625 630 635 640
- Asp Leu Lys Gly Val Tyr Leu Ile Leu Lys Ser Gln Asn Gly Asp Glu 645 650 655
- Ala Trp Gly Asp Asn Phe Ile Ile Leu Glu Ile Ser Pro Ser Glu Lys
 660 665 670
- Leu Leu Ser Pro Glu Leu Ile Asn Thr Asn Asn Trp Thr Ser Thr Gly 675 680 685
- Ser Thr Asn Ile Ser Gly Asn Thr Leu Thr Leu Tyr Gln Gly Gly Arg 690 695 700
- Gly Ile Leu Lys Gln Asn Leu Gln Leu Asp Ser Phe Ser Thr Tyr Arg 705 710 715 720
- Val Tyr Phe Ser Val Ser Gly Asp Ala Asn Val Arg Ile Arg Asn Ser 725 730 735

Arg Glu Val Leu Phe Glu Lys Arg Tyr Met Ser Gly Ala Lys Asp Val 740 745 750

Ser Glu Ile Phe Thr Thr Lys Phe Gly Lys Asp Asn Phe Tyr Ile Glu 755 760 765

Leu Ser Gln Gly Asn Asn Leu Asn Gly Gly Pro Ile Val Gln Phe Pro 770 775 780

Asp Val Ser Ile Lys 785

<210> 7

<211> 2375

<212> DNA

<213> Bacillus thuringiensis

<400> 7

atgaacaaga ataatactaa attaagcaca agagccttac caagttttat tgattatttt 60 aatggcattt atggatttgc cactggtatc aaagacatta tgaacatgat ttttaaaacg 120 gatacaggtg gtgatctaac cctagacgaa attttaaaga atcagcagtt actaaatgat 180 atttctggta aattggatgg ggtgaatgga agcttaaatg atcttatcgc acagggaaac 240 ttaaatacag aattatctaa ggaaatatta aaaattgcaa atgaacaaaa tcaagtttta 300 aatgatgtta ataacaaact cgatgcgata aatacgatgc ttcgggtata tctacctaaa 360 attacctcta tgttgagtga tgtaatgaaa caaaattatg cgctaagtct gcaaatagaa 420 tacttaagta aacaattgca agagatttct gataagttgg atattattaa tgtaaatgta 480 cttattaact ctacacttac tgaaattaca cctgcgtatc aaaggattaa atatgtgaac 540 gaaaaatttg aggaattaac ttttgctaca gaaactagtt caaaagtaaa aaaggatggc 600 tctcctgcag atattcttga tgagttaact gagttaactg aactagcgaa aagtgtaaca 660 aaaaatgatg tggatggttt tgaattttac cttaatacat tccacgatgt aatggtagga 720 aataatttat tegggegtte agetttaaaa aetgeategg aattaattae taaagaaaat 780 gtgaaaacaa gtggcagtga ggtcggaaat gtttataact tcttaattgt attaacagct 840 900 ctgcaagcaa aagcttttct tactttaaca acatgccgaa aattattagg cttagcagat attgattata cttctattat gaatgaacat ttaaataagg aaaaagagga atttagagta 960 aacatcctcc ctacactttc taatactttt tctaatccta attatgcaaa agttaaagga 1020 agtgatgaag atgcaaagat gattgtggaa gctaaaccag gacatgcatt gattgggttt 1080

T:\Sequences\Mycogen\MA-708CDC1\MA-708CDC1.ST25.txt/DNB/ehm

gaaattagta	atgattcaat	tacagtatta	aaagtatatg	aggctaagct	aaaacaaaat	1140
tatcaagtcg	ataaggattc	cttatcggaa	gttatttatg	gtgatatgga	taaattattg	1200
tgcccagatc	aatctgaaca	aatctattat	acaaataaca	tagtatttcc	aaatgaatat	1260
gtaattacta	aaattgattt	cactaaaaaa	atgaaaactt	taagatatga	ggtaacagcg	1320
aatttttatg	attcttctac	aggagaaatt	gacttaaata	agaaaaagt	agaatcaagt	1380
gaagcggagt	atagaacgtt	aagtgctaat	gatgatgggg	tgtatatgcc	gttaggtgtc	1440
atcagtgaaa	catttttgac	tccgattaat	gggtttggcc	tccaagctga	tgaaaattca	1500
agattaatta	ctttaacatg	taaatcatat	ttaagagaac	tactgctagc	aacagactta	1560
agcaataaag	aaactaaatt	gatygtcccg	ccaagtggtt	ttattagcaa	tattgtagag	1620
aacgggtcca	tagaagagga	caatttagag	ccgtgġaaag	caaataataa	gaatgcgtat	1680
gtagatcata	caggcggagt	gaatggaact	aaagctttat	atgttcataa	ggacggagga	1740
atttcacaat	ttattggaga	taagttaaaa	ccgaaaactg	agtatgtaat	ccaatatact	1800
gttaaaggaa	aaccttctat	tcatttaaaa	gatgaaaata	ctggatatat	tcattatgaa	1860
gatacaaata	ataatttaga	agattatcaa	actattaata	aacgttttac	tacaggaact	1920
gatttaaagg	gagtgtattt	aattttaaaa	agtcaaaatg	gagatgaagc	ttggggagat	1980
aactttatta	ttttggaaat	tagtccttct	gaaaagttat	taagtccaga	attaattaat	2040
acaaataatt	ggacgagtac	gggatcaact	aatattagcg	gtaatacact	cactctttat	2100
cagggaggac	gagggattct	aaaacaaaac	cttcaattag	atagtttttc	aacttataga	2160
gtgtatttt	ctgtgtccgg	agatgctaat	gtaaggatta	gaaattctag	ggaagtgtta	2220
tttgaaaaaa	gatatatgag	cggtgctaaa	gatgtttctg	aaatgttcac	tacaaaattt	2280
gagaaagata	acttttatat	agagctttct	caagggaata	atttatatgg	tggtcctatt	2340
gtacattttt	acgatgtctc	tattaagtaa	cccaa			2375

<210> 8

<211> 790

<212> PRT

<213> Bacillus thuringiensis

<400> 8

Met Asn Lys Asn Asn Thr Lys Leu Ser Thr Arg Ala Leu Pro Ser Phe 1 5 . 10 15

Ile Asp Tyr Phe Asn Gly Ile Tyr Gly Phe Ala Thr Gly Ile Lys Asp 20 25 30

Ile Met Asn Met Ile Phe Lys Thr Asp Thr Gly Gly Asp Leu Thr Leu
35 40 45

Asp Glu Ile Leu Lys Asn Gln Gln Leu Leu Asn Asp Ile Ser Gly Lys 50 55 60

Leu Asp Gly Val Asn Gly Ser Leu Asn Asp Leu Ile Ala Gln Gly Asn 65 70 75 80

Leu Asn Thr Glu Leu Ser Lys Glu Ile Leu Lys Ile Ala Asn Glu Gln 85 90 95

Asn Gln Val Leu Asn Asp Val Asn Asn Lys Leu Asp Ala Ile Asn Thr 100 105 110

Met Leu Arg Val Tyr Leu Pro Lys Ile Thr Ser Met Leu Ser Asp Val 115 120 125

Met Lys Gln Asn Tyr Ala Leu Ser Leu Gln Ile Glu Tyr Leu Ser Lys 130 135 140

Gln Leu Gln Glu Ile Ser Asp Lys Leu Asp Ile Ile Asn Val Asn Val 145 150 155 160

Leu Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln Arg Ile 165 170 175

Lys Tyr Val Asn Glu Lys Phe Glu Glu Leu Thr Phe Ala Thr Glu Thr 180 185 190

Ser Ser Lys Val Lys Lys Asp Gly Ser Pro Ala Asp Ile Leu Asp Glu 195 200 205

Leu Thr Glu Leu Thr Glu Leu Ala Lys Ser Val Thr Lys Asn Asp Val 210 215 220

Asp Gly Phe Glu Phe Tyr Leu Asn Thr Phe His Asp Val Met Val Gly 225 230 235 240

- Asn Asn Leu Phe Gly Arg Ser Ala Leu Lys Thr Ala Ser Glu Leu Ile 245 250 255
- Thr Lys Glu Asn Val Lys Thr Ser Gly Ser Glu Val Gly Asn Val Tyr
 260 265 270
- Asn Phe Leu Ile Val Leu Thr Ala Leu Gln Ala Lys Ala Phe Leu Thr 275 280 285
- Leu Thr Thr Cys Arg Lys Leu Leu Gly Leu Ala Asp Ile Asp Tyr Thr 290 295 300
- Ser Ile Met Asn Glu His Leu Asn Lys Glu Lys Glu Glu Phe Arg Val 305 310 315 320
- Asn Ile Leu Pro Thr Leu Ser Asn Thr Phe Ser Asn Pro Asn Tyr Ala 325 330 335
- Lys Val Lys Gly Ser Asp Glu Asp Ala Lys Met Ile Val Glu Ala Lys 340 345 350
- Pro Gly His Ala Leu Ile Gly Phe Glu Ile Ser Asn Asp Ser Ile Thr 355 360 365
- Val Leu Lys Val Tyr Glu Ala Lys Leu Lys Gln Asn Tyr Gln Val Asp 370 380
- Lys Asp Ser Leu Ser Glu Val Ile Tyr Gly Asp Met Asp Lys Leu Leu 385 390 395 400
- Cys Pro Asp Gln Ser Glu Gln Ile Tyr Tyr Thr Asn Asn Ile Val Phe 405 410 415
- Pro Asn Glu Tyr Val Ile Thr Lys Ile Asp Phe Thr Lys Lys Met Lys 420 425 430
- Thr Leu Arg Tyr Glu Val Thr Ala Asn Phe Tyr Asp Ser Ser Thr Gly
 435 440 445
- Glu Ile Asp Leu Asn Lys Lys Lys Val Glu Ser Ser Glu Ala Glu Tyr 450 455 460

Arg Thr Leu Ser Ala Asn Asp Asp Gly Val Tyr Met Pro Leu Gly Val 465 470 475 480

Ile Ser Glu Thr Phe Leu Thr Pro Ile Asn Gly Phe Gly Leu Gln Ala 485 490 495

Asp Glu Asn Ser Arg Leu Ile Thr Leu Thr Cys Lys Ser Tyr Leu Arg
500 505 510

Glu Leu Leu Leu Ala Thr Asp Leu Ser Asn Lys Glu Thr Lys Leu Ile 515 520 525

Val Pro Pro Ser Gly Phe Ile Ser Asn Ile Val Glu Asn Gly Ser Ile 530 540

Glu Glu Asp Asn Leu Glu Pro Trp Lys Ala Asn Asn Lys Asn Ala Tyr 545 550 555 560

Val Asp His Thr Gly Gly Val Asn Gly Thr Lys Ala Leu Tyr Val His
565 570 575

Lys Asp Gly Gly Ile Ser Gln Phe Ile Gly Asp Lys Leu Lys Pro Lys 580 585 590

Thr Glu Tyr Val Ile Gln Tyr Thr Val Lys Gly Lys Pro Ser Ile His 595 600 605

Leu Lys Asp Glu Asn Thr Gly Tyr Ile His Tyr Glu Asp Thr Asn Asn 610 615 620

Asn Leu Glu Asp Tyr Gln Thr Ile Asn Lys Arg Phe Thr Thr Gly Thr 625 630 635 640

Asp Leu Lys Gly Val Tyr Leu Ile Leu Lys Ser Gln Asn Gly Asp Glu 645 650 655

Ala Trp Gly Asp Asn Phe Ile Ile Leu Glu Ile Ser Pro Ser Glu Lys
660 665 670

Leu Leu Ser Pro Glu Leu Ile Asn Thr Asn Asn Trp Thr Ser Thr Gly
675 680 685

Ser Thr Asn Ile Ser Gly Asn Thr Leu Thr Leu Tyr Gln Gly Gly Arg 690 695 Gly Ile Leu Lys Gln Asn Leu Gln Leu Asp Ser Phe Ser Thr Tyr Arg 715 705 Val Tyr Phe Ser Val Ser Gly Asp Ala Asn Val Arg Ile Arg Asn Ser Arg Glu Val Leu Phe Glu Lys Arg Tyr Met Ser Gly Ala Lys Asp Val Ser Glu Met Phe Thr Thr Lys Phe Glu Lys Asp Asn Phe Tyr Ile Glu Leu Ser Gln Gly Asn Asn Leu Tyr Gly Gly Pro Ile Val His Phe Tyr Asp Val Ser Ile Lys Pro <210> <211> . 47 <212> DNA <213> Artificial Sequence <220> <223> 158C2 Primer A <400> gctctagaag gaggtaactt atgaacaaga ataatactaa attaagc 47 <210> 10 <211> 2035 DNA <212> <213> Bacillus thuringiensis atgaacaaga ataatactaa attaagcgca agggcctacc gagttttatt gattatttta 60 atggcattta tggatttgcc actggtatca aagacattat gaatatgatt tttaaaacgg 120 atacaggtgg taatctaacc ttagacgaaa tcctaaagaa tcagcagtta ctaaatgaga 180 tttctggtaa attggatggg gtaaatggga gcttaaatga tcttatcgca cagggaaact 240 taaatacaga attagctaag caaatcttaa aagttgcaaa tgaacaaaat caagtttaa 300 atgatgttaa taacaaacta gactgcgata aatacgatgc ttaaaatata tctacctaaa 360

T:\Sequences\Mycogen\MA-708CDC1\MA-708CDC1.ST25.txt/DNB/ehm

attcacatct	atgttaagtg	atgtactgaa	gccaaaatta	tgtgcttaag	tcttgcaaat	420
tggaattacc	tttaagtaac	atctgcacct	tggcaagaaa	tctccgacaa	gctagatatt	480
attaacgtaa	atgtgcttat	taactctacg	cttactgaaa	ttacacctgc	gtatcaacga	540
attaaatatg	tgaatgaaaa	atttgacgat	ttaacttttg	ctacagaaaa	cactttaaaa	600
gtaaaaaagg	atagctctcc	tgctgatatt	cttgacgagt	taactgaatt	aactgaacta	660
gcgaaaagtg	ttacaaaaaa	tgacgtggat	ggttttgaat	tttaccttaa	tacattccat	720
gatgtaatgg	tgggaaataa	tttattcggt	cgttcagctt	taaaaactgc	ttcggaatta	780
attgctaaag	aaaatgtgaa	aacaagtggc	agtgaagtag	gaaatgttta	taatttctta	840
attgtattaa	cagctctaca	agcaaaagct	tttcttactt	taacaacatg	ccgaaaatta	900
ttaggcttag	cagatattga	ttatacttct	atcatgaatg	agcatttaaa	taaggaaaaa	960
gaggaattta	gagtaaacat	ccttcccaca	ctttctaata	ccttttctaa	tcctaattat	1020
gcaaaagcta	agggaagtaa	tgaagataca	aagatgattg	tggaagctaa	accaggatat	1080
gttttggttg	gatttgaaat	gagcaataat	tcaattacag	tattaaaagc	atatcaagct.	1140
aagctaaaaa	aagattatca	aattgataag	gattcgttat	cagaaataat	atatagtacg	1200
tgatacggat	aaattattat	gtccggatca	atctgaacaa	tatattatac	aaagaacata	1260
gcatttccaa	atgaatatgt	tattactaaa	attgctttta	ctaaaaaaat	gaacagttta	1320
aggtatgagg	cgacagcgaa	tttttatgat	tcttctacag	gggatattga	tctaaataag	1380
acaaaagtag	aatcaagtga	agcggagtat	agtatgctaa	aagctagtga	tgatgaagtt	1440
tacatgccgc	taggtcttat	cagtgaaaca	tttttaaatc	caattaatgg	atttaggctt	1500
gcagtcgatg	aaaattccag	actagtaact	ttaacatgta	gatcatattt	aagagagaca	1560
ttgttagcga	cagatttaaa	taataaagaa	actaaattga	ttgtcccacc	taatgttttt	1620
attagcaata	ttgtagagaa	tggaaatata	gaaatggaca	ccttagaacc	atggaaggca	1680
aataatgaga	atgcgaatgt	agattattca	ggcggagtga	atggaactag	agctttatat	1740
gttcataagg	atggtgaatt	ctcacatttt	attggagaca	agttgaaatc	taaaacagaa	1800
tacttgattc	gatatattgt	aaaaggaaaa	gcttctattt	ttttaaaaga	tgaaagaaat	1860
gaaaattaca	tttacgagga	tacaaataat	aatttagaag	attatcaaac	tattactaaa	1920
cgttttacta	caggaactga	ttcgacagga	ttttatttat	tttttactac	tcaagatgga	1980
aatgaagctt	ggggagacac	ttttttctc	tagaaagagg	taacttatga	acaag	2035

<210>	11						
<211>	21						
<212>	DNA						
<213>	Art	ificial Seq	uence				
<220>							
<223>	49C	Primer A		•	٠.,		
<400>	11						
catcct	ccct	acactttcta	a				21
			•				
<210>	12	·					
<211>	950						
<212>	DNA						
<213>	Bac	illus thurin	ngiensis				
<400>	12		•				
aaactag	gagg	gagtgataag	gatgcgaaaa	tcattatgga	agctaaacct	ggatatgctt	60
tagttgg	gatt	tgaaataagt	aaggattcaa	ttgcagtatt	aaaagtttat	caggcaaagc	120
taaaaca	acaa	ctatcaaatt	gataaggatt	cgttatcaga	aattgtttat	ggtgatatag	180
ataaatt	att	atgtccggat	caatctgaac	aaatgtatta	tacaaataaa	atagcatttc	240
					•		
		tgttatcact					300
aggtcac	cagc	gaattttat	gactcttcta	caggagatat	tgatctáaat	aagaaaaaaa	360
tagaato	caag	tgaagcggag	tttagtatgc	taaatgctaa	taatgatggt	gtttatatgc	420
cgatago	gtac	tataagtgaa	acatttttga	ctccaattaa	tggatttggc	ctcgtagtcg	480
atgaaaa	ttc	aagactagta	actttgacat	gtaaatcata	tttaagagag	acattgttag	540
caacaga	ctt	aagtaataaa	gaaactaaac	tgattgtccc	acctaatggt	tttattagca	600
atattgt	aga	aaatgggaac	ttagagggag	aaaacttaga	gccgtgggaa	agcaaataac	660
		atgtagatca					720
gaggacg	laca	agtteteaca	atttattggg	gataaattga	aattgaaaac	agaatatgta	780
attccat	ata	ttgtaaaggg	gaaagctgct	atttatttaa	aagatgaaaa	aaatggggat	840
tacatat	cat	gaagaaacat	cataatgcaa	ttgaagattt	ttccagctgt	aacttcaata	900
atgattt	tcg	catccttatc	atccctctag	ctttttcata.	ataggataga	7 4,	. 950
<210>	13						
<211>	20				•		

<212> DNA

<213> Artificial Sequence

T:\Sequences\Mycogen\MA-708CDC1\MA-708CDC1.ST25.txt/DNB/ehm

<220>							
<223>	49C	Primer B					
<400>	13						
aaatta	tgcg	ctaagtctgc	•				20
<210>	14						
<211>	19	•					
<212>	DNA						
<213>	Arti	ficial Sequ	ience				
<220>					-		
<223>	49C	Primer C					
<400>	14						
		cataataat		•			19
-,-3	-33-	,		•			
				• .			
<210>	15	•		*	•		
<211>	176						
<212>	DNA		•		•		
<213>	Вас	lllus thurin	ngiensis				
<400>	15						
		cgctaagtct	gcaccttttt	tcactottac	taaacatcac	ttttcctata	60
J					•		
tacaat	tagc	tcttatggat	tattgagcaa	acttatcttg	ttaattacta	ctccccatca	120
				•		•	
tatgct	aaac	aaaaaccaaa	caaacattat	ctattatatg	tccggatcaa	aatgta	176
<210>	16					•	
<211>	236	L				•	
<212>	DNA	,	•				
<213>	Bac	illus thurir	ngiensis		•		
<400>	16					*****	C 0
atgcaa	aaaa	ataataaatt	aagtgtaaag	gctttaccaa	gtttcattga	ttattttaat	60
ggaatt	taco	gattcgccac	tootatcaaa	gatattatga	acatgatttt	taaaacgaat	120
994400	. د مت	5000050000	0990000000	guouoouogu			
acagga	gggg	atctaacctt	agacgaaata	ttaaaaaatc	aacagttact	taatgagatt	180
tctggc	aaac	tggatggagt	gaatggcagc	ttaaatgatc	ttctcgcaca	aggaaacttg	240
gatact	gaat	tatctaagga	aatattaaaa	attgcaaatg	aacagaataa	ggttttaaat	300
astats	aata	caaagcttga	tacastssst	ttaatoctta	acacatattt	acctaaaatt	360
gacgca	uaca	caaageeega	cycyacaaac	ccaacyccca	acacacacc	acceaaaac	500
acttct	atgt	taagtgatgt	aatgaaacaa	aattatgcat	taggtttgca	aatagaatac	420
	_			-	, -	-	
ctaago	aaac	aattaaagga	aatttcagat	aagctagatg	ttattaatgt	aaatgtactc	480
						.	
attaac	tcta	cacttactga	aattacacct	gcctatcaaa	ggattaaata	tgtaaatgaa	540
222+++	מפפת	cattaacctc	tactacacaa	accaatttaa	aaacabaaca	agatagetet	600
uaattt	.yaay	Callaactic	cyccacayaa	accuactiaa	uuuvuuaaca	agacagecee	500

T:\Sequences\Mycogen\MA-708CDC1\MA-708CDC1.ST25.txt/DNB/ehm

catacagata ttcttgatga gttaacagag ctaacggaac tagcgaaaag tgtaacaaaa 660 aatgacgtgg atggctttga attttacctt aatacattcc acgatgtaat gattgggaat 720 780 aatctatttg gacgttcagc tttaaaaaca gcctcggaat taattgcgaa agaaaatttg 840 aaaacaagtg gcagtgaggt aggaaatgtt tataatttct taattgtatt aacagctctg 900 caagcaaaag cttttcttac tttaactaca tgccggaaat tattgggctt agcagatatt 960 gattatactc ctattatgaa tgaacaccta aataaagaaa aagaggaatt tagagtgaac 1020 atccttccta cactttctaa tactttttct aatcctaatt atgaaaaagc tagagggagt 1080 gataaggatg cgaaaatcat tatggaagct aaacctggat atgctttagt tggatttgaa 1140 ataagtaagg attcaattgc agtattaaaa gtttatcagg caaagctaaa acacaactat 1200 caaattgata aggattcgtt atcagaaatt gtttatggtg atatagataa attattatgt ccggatcaat ctgaacaaat gtattataca aataaaatag catttccaaa tgaatatgtt 1260 1320 atcactaaaa ttgcttttac taaaaaactg aacagtttaa gatatgaggt cacagcgaat 1380 ttttatgact cttctacagg agatattgat ctaaataaga aaaaaataga atcaagtgaa gcggagttta gtatgctaaa tgctaataat gatggtgttt atatgccgat aggtactata 1440 1500 agtgaaacat ttttgactcc aattaatgga tttggcctcg tagtcgatga aaattcaaga ctagtaactt tgacatgtaa atcatattta agagagacat tgttagcaac agacttaagt 1560 1620 aataaagaaa ctaaactgat tgtcccacct aatggtttta ttagcaatat tgtagaaaat 1680 gggaacttag agggagaaa cttagagccg tggaaagcaa ataacaaaaa tgcgtatgta 1740 gatcataccg gaggtgtaaa tggaactaaa gttttatatg ttcatgagga tggtgagttc 1800 tcacaattta ttggggataa attgaaattg aaaacagaat atgtaattca atatattgta 1860 aagggaaaag ctgctattta tttaaaagat gaaaaaaatg gggattacat ttatgaagaa acaaataatg aattagaaga ttttcaagct gttactaaac gttttattac gggaacagat 1920 tetteaagag tteatttaat ttttaecagt caaaatggeg aggaageatt tggaggaaac 1980 2040 tttattattt cagaaattag gccatccgaa gagttattaa gtccagaatt gattaagtcg gatgettggg ttggatetea gggaaettgg ateteaggaa atteteteaa tattaatagt 2100 aatgtaaatg gaacctttcg acaaaacctt tcgttagaaa gttattcaac ctatagtatg 2160 2220 aactttaatg tgaatggatt tggcaaggtg acaataagaa attctcgtga agtagtattt gaaaggagtt atctacagtt ttcctctaaa tatatttcag aaaaattcac aacaacaacc 2280 aataatactg ggttatatgt agaactttct cgtgcttcgt ctaggggagt tataaatttc 2340 ggagattttt caatcaagta a 2361

<210> 17

<211> 786

<212> PRT

<213> Bacillus thuringiensis

<400> 17

Met Gln Lys Asn Asn Lys Leu Ser Val Lys Ala Leu Pro Ser Phe Ile 1 5 10 15

Asp Tyr Phe Asn Gly Ile Tyr Gly Phe Ala Thr Gly Ile Lys Asp Ile
20 25 30

Met Asn Met Ile Phe Lys Thr Asn Thr Gly Gly Asp Leu Thr Leu Asp 35 40 45

Glu Ile Leu Lys Asn Gln Gln Leu Leu Asn Glu Ile Ser Gly Lys Leu 50 55 60

Asp Gly Val Asn Gly Ser Leu Asn Asp Leu Leu Ala Gln Gly Asn Leu 65 70 75 80

Asp Thr Glu Leu Ser Lys Glu Ile Leu Lys Ile Ala Asn Glu Gln Asn 85 90 95

Lys Val Leu Asn Asp Val Asn Thr Lys Leu Asp Ala Ile Asn Leu Met 100 105 110

Leu Asn Thr Tyr Leu Pro Lys Ile Thr Ser Met Leu Ser Asp Val Met 115 120 125

Lys Gln Asn Tyr Ala Leu Gly Leu Gln Ile Glu Tyr Leu Ser Lys Gln 130 135 140

Leu Lys Glu Ile Ser Asp Lys Leu Asp Val Ile Asn Val Asn Val Leu 145 150 155 160

Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln Arg Ile Lys 165 170 175

- Tyr Val Asn Glu Lys Phe Glu Ala Leu Thr Ser Ala Thr Glu Thr Asn 180 185 190
- Leu Lys Thr Lys Gln Asp Ser Ser His Thr Asp Ile Leu Asp Glu Leu 195 200 205
- Thr Glu Leu Thr Glu Leu Ala Lys Ser Val Thr Lys Asn Asp Val Asp 210 215 220
- Gly Phe Glu Phe Tyr Leu Asn Thr Phe His Asp Val Met Ile Gly Asn 225 230 235 240
- Asn Leu Phe Gly Arg Ser Ala Leu Lys Thr Ala Ser Glu Leu Ile Ala 245 250 255
- Lys Glu Asn Leu Lys Thr Ser Gly Ser Glu Val Gly Asn Val Tyr Asn 260 265 270
- Phe Leu Ile Val Leu Thr Ala Leu Gln Ala Lys Ala Phe Leu Thr Leu 275 280 285
- Thr Thr Cys Arg Lys Leu Leu Gly Leu Ala Asp Ile Asp Tyr Thr Pro 290 295 300
- Ile Met Asn Glu His Leu Asn Lys Glu Lys Glu Glu Phe Arg Val Asn 305 310 315 320
- Ile Leu Pro Thr Leu Ser Asn Thr Phe Ser Asn Pro Asn Tyr Glu Lys 325 330 335
- Ala Arg Gly Ser Asp Lys Asp Ala Lys Ile Ile Met Glu Ala Lys Pro 340 345 350
- Gly Tyr Ala Leu Val Gly Phe Glu Ile Ser Lys Asp Ser Ile Ala Val 355 360 365
- Leu Lys Val Tyr Gln Ala Lys Leu Lys His Asn Tyr Gln Ile Asp Lys 370 380
- Asp Ser Leu Ser Glu Ile Val Tyr Gly Asp Ile Asp Lys Leu Leu Cys 385 390 395 400

- Pro Asp Gln Ser Glu Gln Met Tyr Tyr Thr Asn Lys Ile Ala Phe Pro 405 410 415
- Asn Glu Tyr Val Ile Thr Lys Ile Ala Phe Thr Lys Lys Leu Asn Ser 420 425 430
- Leu Arg Tyr Glu Val Thr Ala Asn Phe Tyr Asp Ser Ser Thr Gly Asp
 435 440 445
- Ile Asp Leu Asn Lys Lys Lys Ile Glu Ser Ser Glu Ala Glu Phe Ser 450 455 460
- Met Leu Asn Ala Asn Asn Asp Gly Val Tyr Met Pro Ile Gly Thr Ile 465 470 475 480
- Ser Glu Thr Phe Leu Thr Pro Ile Asn Gly Phe Gly Leu Val Val Asp 485 490 495
- Glu Asn Ser Arg Leu Val Thr Leu Thr Cys Lys Ser Tyr Leu Arg Glu 500 505 510
- Thr Leu Leu Ala Thr Asp Leu Ser Asn Lys Glu Thr Lys Leu Ile Val 515 520 525
- Pro Pro Asn Gly Phe Ile Ser Asn Ile Val Glu Asn Gly Asn Leu Glu 530 540
- Gly Glu Asn Leu Glu Pro Trp Lys Ala Asn Asn Lys Asn Ala Tyr Val 545 550 555 560
- Asp His Thr Gly Gly Val Asn Gly Thr Lys Val Leu Tyr Val His Glu 565 570 575
- Asp Gly Glu Phe Ser Gln Phe Ile Gly Asp Lys Leu Lys Leu Lys Thr 580 585 590
- Glu Tyr Val Ile Gln Tyr Ile Val Lys Gly Lys Ala Ala Ile Tyr Leu 595 600 605
- Lys Asp Glu Lys Asn Gly Asp Tyr Ile Tyr Glu Glu Thr Asn Asn Glu 610 620

625	GIU	nsp	rne	GIII	630	vai	1111	цур	Arg	635	110	****	GLY	1111	640	
Ser	Ser	Arg	Val	His 645	Leu	Ile	Phe	Thr	Ser 650	Gln	Asn	Gly	Glu	Glu 655	Ala	
Phe	Gly	Gly	Asn 660	Phe	Ile	Ile	Ser	Glu 665	Ile	Arg	Pro	Ser	Glu 670	Glu	Leu	
Leu	Ser	Pro 675	Glu	Leu	Ile	Lys	Ser 680	Asp	Ala	Trp	Val	Gly 685	Ser	Gln	Gly	
Thr	Trp 690	Ile	Ser	Gly		Ser 695	Leu	Asn	Ile	Asn	Ser 700	Asn	Val	Asn	Gly	
Thr 705	Phe	Arg	Gln	Asn	Leu 710	Ser	Leu	Glu	Ser	Tyr 715	Ser	Thr	Tyr	Ser	Met 720	
Asn	Phe	Asn	Val	Asn 725	_	Phe	Gly	Lys	Val 730		Ile	Arg		Ser 735	Arg	•
Glu	Val	Val	Phe 740	Glu	Arg	Ser	Tyr	Leu 745	Gln	Phe	Ser	Ser	Lys 750	Tyr	Ile	
Ser	Glu	Lys 755	Phe	Thr	Thr	Thr	Thr 760	Asn	Asn	Thr	Gly	Leu 765	Tyr	Val	Glu	
Leu	Ser 770	Arg	Ala	Ser	Ser	Arg 775	Gly	Val	Ile		Phe 780	Gly	Asp	Phe	Ser	
Ile 785	Lys						·			•						
<210 <210 <210 <210	1> : 2> :	18 2361 DNA Baci	llus	thu	ring	iens	is									
<400		18 tga a	ataa	tact	aa a	ttaa	acgc	a ag	aacc	ctac	cgae	attt	tat	tgati	tatttt	6(
															aaaacg	
														•	aatgag	
att	tctg	gta (aatt	ggat	gg g	gtaa	atgg	g ag	ctta	aatg	atc	ttat	cgc	acag	ggaaac	240

T:\Sequences\Mycogen\MA-708CDC1\MA-708CDC1.ST25.txt/DNB/ehm

ttaaatacag aattagctaa gcaaatctta aaagttgcaa atgaacaaaa tcaagtttta 300 aatgatgtta ataacaaact agatgcgata aattcgatgc ttaaaatata tctacctaaa 360 attacatcta tgttaagtga tgtaatgaag caaaattatg tgctaagctt gcaaatagaa 420 tacttaagta aacaattgca agaaatctcc gacaagctag atattattaa cgtaaatgtg 480 cttattaact ctacgcttac tgaaattaca cctgcgtatc aacgaattaa atatgtgaat 540 gaaaaaatttg acgatttaac ttttgctaca gaaaacactt taaaagtaaa aaaggatagc 600 tctcctgctg atattcttga cgagttaact gaattaactg aactagcgaa aagtgttaca 660 aaaaatgacg tggatggttt tgaattttac cttaatacat tccatgatgt aatggtggga 720 aataatttat teggtegtte agetttaaaa aetgettegg aattaattge taaagaaaat 780 840 gtgaaaacaa gtggcagtga agtaggaaat gtttataatt tcttaattgt attaacagct ctacaagcaa aagcttttct tactttaaca acatgccgaa aattattagg cttagcagat 900 960 attgattata cttctatcat gaatgagcat ttaaataagg aaaaagagga atttagagta aacateette ecacaettte taataeettt tetaateeta attatgeaaa agetaaggga 1020 agtaatgaag atacaaagat gattgtggaa gctaaaccag gatatgtttt ggttggattt 1080 1140 1200 tatcaaattg ataaggattc gttatcagaa ataatatata gtgatacgga taaattatta 1260 tgtccggatc aatctgaaca aatatattat acaaagaaca tagcatttcc aaatgaatat gttattacta aaattgcttt tactaaaaaa atgaacagtt taaggtatga ggcgacagcg 1320 aatttttatg attcttctac aggggatatt gatctaaata agacaaaagt agaatcaagt 1380 gaagcggagt atagtatgct aaaagctagt gatgatgaag tttacatgcc gctaggtctt 1440 1500 atcagtgaaa catttttaaa tccaattaat ggatttaggc ttgcagtcga tgaaaattcc agactagtaa ctttaacatg tagatcatat ttaagagaga cattgttagc gacagattta 1560 aataataaag aaactaaatt gattgtccca cctaatgttt ttattagcaa tattgtagag 1620 aatggaaata tagaaatgga caccttagaa ccatggaagg caaataatga gaatgcgaat 1680 1740 gtagattatt caggcggagt gaatggaact agagctttat atgttcataa ggatggtgaa ttctcacatt ttattggaga caagttgaaa tctaaaacag aatacttgat tcgatatatt 1800 1860 gtaaaaggaa aagcttctat ttttttaaaa gatgaaaaaa atgaaaatta catttacgag 1920 gatacaaata ataatttaga agattatcaa actattacta aacgttttac tacaggaact

gattcgacag	gagtttattt	aatttttaat	agtcaaaatg	gagatgaagc	ttggggagat	1980
aactttatta	ttttggaaat	tagtccgtgt	gaaaagttat	taagtccaga	attaattaaa	2040
acagataaat	ggattagtac	gggatcgact	tatattagcg	atgatagact	cactctttat	2100
cagggaggac	gaggaatttt	aaagcaaaac	cttcaattag	atcgttttc	aacttataga	2160
gtcaattttt	ctgtgaacgg	agatgctaat	gtaaggattc	gtaattctag	ggaagtgtta	2220
cttgaaaaaa	gatatttgaa	ccgtaaaggt	gtttctgaaa	tgttcactac	aaaatttgat	2280
aaagataact	tttatgtaga	gctttctcaa	ggggataatc	ttggtactgt	tgtacatttt	2340
tatgatttct	ctattaaata	a				2361

<210> 19

<211> 786

<212> PRT

<213> Bacillus thuringiensis

<400> 19

Met Asn Met Asn Asn Thr Lys Leu Asn Ala Arg Ala Leu Pro Ser Phe 1 5 10 15

Ile Asp Tyr Phe Asn Gly Ile Tyr Gly Phe Ala Thr Gly Ile Lys Asp

Ile Met Asn Met Ile Phe Lys Thr Asp Thr Gly Gly Asn Leu Thr Leu 35 40 45

Asp Glu Ile Leu Lys Asn Gln Gln Leu Leu Asn Glu Ile Ser Gly Lys 50 55 60

Leu Asp Gly Val Asn Gly Ser Leu Asn Asp Leu Ile Ala Gln Gly Asn 65 70 75 80

Leu Asn Thr Glu Leu Ala Lys Gln Ile Leu Lys Val Ala Asn Glu Gln 85 90 95

Asn Gln Val Leu Asn Asp Val Asn Asn Lys Leu Asp Ala Ile Asn Ser 100 105 110

Met Leu Lys Ile Tyr Leu Pro Lys Ile Thr Ser Met Leu Ser Asp Val 115 120 125

Met	Lys	Gln	Asn	Tyr	Val	Leu	Ser	Leu	Gln	Ile	Glu	Tyr	Leu	Ser	Lys
	130					135					140				

Gln Leu Gln Glu Ile Ser Asp Lys Leu Asp Ile Ile Asn Val Asn Val 145 150 155 '. 160

Leu Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln Arg Ile 165 170 175

Lys Tyr Val Asn Glu Lys Phe Asp Asp Leu Thr Phe Ala Thr Glu Asn 180 185 190

Thr Leu Lys Val Lys Lys Asp Ser Ser Pro Ala Asp Ile Leu Asp Glu
195 200 205

Leu Thr Glu Leu Thr Glu Leu Ala Lys Ser Val Thr Lys Asn Asp Val 210 215 220

Asp Gly Phe Glu Phe Tyr Leu Asn Thr Phe His Asp Val Met Val Gly 225 230 235 240

Asn Asn Leu Phe Gly Arg Ser Ala Leu Lys Thr Ala Ser Glu Leu Ile 245 250 255

Ala Lys Glu Asn Val Lys Thr Ser Gly Ser Glu Val Gly Asn Val Tyr
260 265 270

Asn Phe Leu Ile Val Leu Thr Ala Leu Gln Ala Lys Ala Phe Leu Thr 275 280 285

Leu Thr Thr Cys Arg Lys Leu Leu Gly Leu Ala Asp Ile Asp Tyr Thr 290 295 300

Ser Ile Met Asn Glu His Leu Asn Lys Glu Lys Glu Glu Phe Arg Val 305 310 315 320

Asn Ile Leu Pro Thr Leu Ser Asn Thr Phe Ser Asn Pro Asn Tyr Ala 325 330 335

Lys Ala Lys Gly Ser Asn Glu Asp Thr Lys Met Ile Val Glu Ala Lys 340 345 350

- Pro Gly Tyr Val Leu Val Gly Phe Glu Met Ser Asn Asn Ser Ile Thr 355 360 365
- Val Leu Lys Ala Tyr Gln Ala Lys Leu Lys Lys Asp Tyr Gln Ile Asp 370 380
- Lys Asp Ser Leu Ser Glu Ile Ile Tyr Ser Asp Thr Asp Lys Leu Leu 385 390 395 400
- Cys Pro Asp Gln Ser Glu Gln Ile Tyr Tyr Thr Lys Asn Ile Ala Phe
 405 410 415
- Pro Asn Glu Tyr Val Ile Thr Lys Ile Ala Phe Thr Lys Lys Met Asn 420 425 430
- Ser Leu Arg Tyr Glu Ala Thr Ala Asn Phe Tyr Asp Ser Ser Thr Gly
 435 440 445
- Asp Ile Asp Leu Asn Lys Thr Lys Val Glu Ser Ser Glu Ala Glu Tyr 450 455 460
- Ser Met Leu Lys Ala Ser Asp Asp Glu Val Tyr Met Pro Leu Gly Leu 465 470 475 480
- Ile Ser Glu Thr Phe Leu Asn Pro Ile Asn Gly Phe Arg Leu Ala Val 485 490 495
- Asp Glu Asn Ser Arg Leu Val Thr Leu Thr Cys Arg Ser Tyr Leu Arg 500 505 510
- Glu Thr Leu Leu Ala Thr Asp Leu Asn Asn Lys Glu Thr Lys Leu Ile 515 520 525
- Val Pro Pro Asn Val Phe Ile Ser Asn Ile Val Glu Asn Gly Asn Ile 530 535 540
- Glu Met Asp Thr Leu Glu Pro Trp Lys Ala Asn Asn Glu Asn Ala Asn 545 555 560
- Val Asp Tyr Ser Gly Gly Val Asn Gly Thr Arg Ala Leu Tyr Val His 565 570 575

Lys Asp Gly Glu Phe Ser His Phe Ile Gly Asp Lys Leu Lys Ser Lys 580 585 590

Thr Glu Tyr Leu Ile Arg Tyr Ile Val Lys Gly Lys Ala Ser Ile Phe 595 600 605

Leu Lys Asp Glu Lys Asn Glu Asn Tyr Ile Tyr Glu Asp Thr Asn Asn 610 620

Asn Leu Glu Asp Tyr Gln Thr Ile Thr Lys Arg Phe Thr Thr Gly Thr 625 630 635 640

Asp Ser Thr Gly Val Tyr Leu Ile Phe Asn Ser Gln Asn Gly Asp Glu 645 650 655

Ala Trp Gly Asp Asn Phe Ile Ile Leu Glu Ile Ser Pro Cys Glu Lys
660 665 670

Leu Leu Ser Pro Glu Leu Ile Lys Thr Asp Lys Trp Ile Ser Thr Gly
675 680 685

Ser Thr Tyr Ile Ser Asp Asp Arg Leu Thr Leu Tyr Gln Gly Gly Arg 690 695 700

Gly Ile Leu Lys Gln Asn Leu Gln Leu Asp Arg Phe Ser Thr Tyr Arg 705 710 715 720

Val Asn Phe Ser Val Asn Gly Asp Ala Asn Val Arg Ile Arg Asn Ser 725 730 735

Arg Glu Val Leu Leu Glu Lys Arg Tyr Leu Asn Arg Lys Gly Val Ser 740 745 750

Glu Met Phe Thr Thr Lys Phe Asp Lys Asp Asn Phe Tyr Val Glu Leu 755 760 765

Ser Gln Gly Asp Asn Leu Gly Thr Val Val His Phe Tyr Asp Phe Ser 770 775 780

Ile Lys 785

<210> 20

4.

```
<211> 17
<212> DNA
<213> Artificial Sequence
<220>
<223> SUP-1A forward primer
<400> 20
                                                                     17
ggattcgtta tcagaaa
<210> 21
<211>
      17
<212> DNA
<213> Artificial Sequence
<220>
<223> SUP-1B reverse primer
<400> 21
                                                                      17
ctgtygctaa caatgtc
<210> 22
<211> 47
<212> DNA
<213> Artificial Sequence
<220>
<223> SUP primer
<400> 22
                                                                      47
gctctagaag gaggtaactt atgaacaaga ataatactaa attaagc
<210>
      23
<211> 27
<212> DNA
<213> Artificial Sequence
<220>
<223> SUP primer
<400> 23
ggggtacctt acttaataga gacatcg
                                                                      27
<210> 24
<211>
       2364
<212> DNA
<213> Bacillus thuringiensis
<400> 24
atgaatatga ataatactaa attaaacgca agggccctac cgagttttat tgattatttt
aatggcattt atggatttgc cactggtatc aaagacatta tgaatatgat ttttaaaacg
                                                                     120
```

gatacaggtg gtaatctaac cttagacgaa atcctaaaga atcagcagtt actaaatgag 180 atttctggta aattggatgg ggtaaatggg agcttaaatg atcttatcgc acagggaaac 300 ttaaatacag aattatctaa ggaaatctta aaaattgcaa atgaacagaa tcaagtctta aatgatgtta ataacaaact cgatgcgata aatacgatgc ttcatatata tctacctaaa 360 atcacatcta tgttaagtga tgtaatgaag caaaattatg cgctaagtct gcaagtagaa 420 tacttaagta aacaattgaa agaaatttct gataaattag atgttattaa cgtaaatgtt 480 cttattaact ctacacttac tgaaattaca cctgcatatc aacggattaa atatgtaaat 540 gaaaaatttg aagaattaac ttttgctaca gaaaccactt taaaagtaaa aaaggatagc 600 tegeetgetg atattettga egagttaaet gaattaaetg aactagegaa aagtgttaea 660 aaaaatgacg tggatggttt tgaattttac cttaatacat tccacgatgt aatggtagga 720 aataatttat tcgggcgttc agctttaaaa actgcttcag aattaattgc taaagaaaat 780 gtgaaaacaa gtggcagtga agtaggaaat gtttataatt tcttaattgt attaacagct 840 ctacaagcaa aagcttttct tactttaaca acatgccgaa aattattagg cttagcagat 900 attgattata catctattat gaatgaacat ttaaataagg aaaaagagga atttagagta 960 aacatccttc ctacactttc taatactttt tctaatccta attatgcaaa agttaaagga 1020 1080 agtgatgaag atgcaaagat gattgtggaa gctaaaccag gacatgcatt ggttgggttt 1140 1200 taccaagttg ataaggattc cttatcggaa gtcatttata gtgatatgga taaattattg tgcccagatc aatctgaaca aatttattat acaaataata tagtatttcc aaatgaatat 1260 gtaattacta aaattgattt tactaagaaa atgaaaactt taagatatga ggtaacagct 1320 aattettaeg attettetae aggagaaatt gaettaaata agaagaaagt agaateaagt 1380 gaageggagt ataggaegtt aagtgetaat aatgatggag tatatatgee gttaggtgte . 1440 1500 atcagtgaaa catttttgac tecaattaat ggatttggec tecaagetga tgaaaattea 1560 agattaatta ctttaacatg taaatcatat ttaagggaac tactactagc gacagactta 1620 agcaataaag aaactaaatt gattgtcccg cctattagtt ttattagtaa tattgtagaa aatgggaact tagagggaga aaacttagag ccgtggatag caaataacaa aaatgcgtat 1680 1740 gtagatcata caggtggtat aaatggaact aaagttttat atgttcataa ggatggtgag 1800 ttttcacaat ttgttggagg taagttaaaa tcgaaaacag aatatgtaat tcaatatat 1860 gtaaagggaa aagcttctat ttatttaaaa gataaaaaaa atgagaattc catttatgaa

T:\Sequences\Mycogen\MA-708CDC1\MA-708CDC1.ST25.txt/DNB/ehm

gaaataaata	atgatttaga	aggttttcaa	actgttacta	aacgttttat	tacaggaacg	1920
gattcttcag	ggattcattt	aatttttacc	agtcaaaatg	gcgagggagc	atttggagga	1980
aactttatta	tctcagaaat	taggacatcc	gaagagttat	taagtccaga	attgattatg	2040
tcggatgctt	gggttggatc	ccagggaact	tggatctcag	gaaattctct	cactattaat	2100
agtaatgtaa	atggaacctt	tcgacaaaat	cttccgttag	aaagttattc	aacctatagt	2160
atgaacttta	ctgtgaatgg	atttggcaag	gtgacagtaa	gaaattctcg	tgaagtatta	2220
tttgaaaaaa	gttatccgca	gctttcacct	aaagatattt	ctgaaaaatt	tacaactgca	2280
gccaataata	ccggattata	tgtagagctt	tctcgctcaa	cgtcgggtgg	tgcaataaat	2340
ttccgagatt	tttcaattaa	gtaa		•		2364

<210> 25

<211> 787

<212> PRT

<213> Bacillus thuringiensis

<400> 25

Met Asn Met Asn Asn Thr Lys Leu Asn Ala Arg Ala Leu Pro Ser Phe 1 5 10 15

Ile Asp Tyr Phe Asn Gly Ile Tyr Gly Phe Ala Thr Gly Ile Lys Asp 20 . 25 30

Ile Met Asn Met Ile Phe Lys Thr Asp Thr Gly Gly Asn Leu Thr Leu 35 40 45

Asp Glu Ile Leu Lys Asn Gln Gln Leu Leu Asn Glu Ile Ser Gly Lys 50 55 60

Leu Asp Gly Val Asn Gly Ser Leu Asn Asp Leu Ile Ala Gln Gly Asn 65 70 75 80

Leu Asn Thr Glu Leu Ser Lys Glu Ile Leu Lys Ile Ala Asn Glu Gln 85 90 95

Asn Gln Val Leu Asn Asp Val Asn Asn Lys Leu Asp Ala Ile Asn Thr 100 105 110

Met Leu His Ile Tyr Leu Pro Lys Ile Thr Ser Met Leu Ser Asp Val

Met Lys Gln Asn Tyr Ala Leu Ser Leu Gln Val Glu Tyr Leu Ser Lys 130 135 140

Gln Leu Lys Glu Ile Ser Asp Lys Leu Asp Val Ile Asn Val Asn Val 145 150 155 160

Leu Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln Arg Ile 165 170 175

Lys Tyr Val Asn Glu Lys Phe Glu Glu Leu Thr Phe Ala Thr Glu Thr 180 185 190

Thr Leu Lys Val Lys Lys Asp Ser Pro Ala Asp Ile Leu Asp Glu 195 200 205

Leu Thr Glu Leu Thr Glu Leu Ala Lys Ser Val Thr Lys Asn Asp Val 210 215 220

Asp Gly Phe Glu Phe Tyr Leu Asn Thr Phe His Asp Val Met Val Gly 225 230 235 240

Asn Asn Leu Phe Gly Arg Ser Ala Leu Lys Thr Ala Ser Glu Leu Ile 245 250 255

Ala Lys Glu Asn Val Lys Thr Ser Gly Ser Glu Val Gly Asn Val Tyr 260 265 270

Asn Phe Leu Ile Val Leu Thr Ala Leu Gln Ala Lys Ala Phe Leu Thr 275 280 285

Leu Thr Thr Cys Arg Lys Leu Leu Gly Leu Ala Asp Ile Asp Tyr Thr 290 295 300

Ser Ile Met Asn Glu His Leu Asn Lys Glu Lys Glu Glu Phe Arg Val 305 310 315 320

Asn Ile Leu Pro Thr Leu Ser Asn Thr Phe Ser Asn Pro Asn Tyr Ala 325 330 335

Lys Val Lys Gly Ser Asp Glu Asp Ala Lys Met Ile Val Glu Ala Lys
340 345 350

- Pro Gly His Ala Leu Val Gly Phe Glu Ile Ser Asn Asp Ser Met Thr 355 360 365
- Val Leu Lys Val Tyr Glu Ala Lys Leu Lys Gln Asn Tyr Gln Val Asp 370 375 380
- Lys Asp Ser Leu Ser Glu Val Ile Tyr Ser Asp Met Asp Lys Leu Leu 385, 390 395 400
- Cys Pro Asp Gln Ser Glu Gln Ile Tyr Tyr Thr Asn Asn Ile Val Phe 405 410 415
- Pro Asn Glu Tyr Val Ile Thr Lys Ile Asp Phe Thr Lys Lys Met Lys
 420 425 430
- Thr Leu Arg Tyr Glu Val Thr Ala Asn Ser Tyr Asp Ser Ser Thr Gly
 435 440 445
- Glu Ile Asp Leu Asn Lys Lys Lys Val Glu Ser Ser Glu Ala Glu Tyr 450 455 460
- Arg Thr Leu Ser Ala Asn Asn Asp Gly Val Tyr Met Pro Leu Gly Val 465 470 475 480
- Ile Ser Glu Thr Phe Leu Thr Pro Ile Asn Gly Phe Gly Leu Gln Ala
 485
 490
 495
- Asp Glu Asn Ser Arg Leu Ile Thr Leu Thr Cys Lys Ser Tyr Leu Arg
 500 505 510
- Glu Leu Leu Leu Ala Thr Asp Leu Ser Asn Lys Glu Thr Lys Leu Ile 515 520 525
- Val Pro Pro Ile Ser Phe Ile Ser Asn Ile Val Glu Asn Gly Asn Leu 530 540
- Glu Gly Glu Asn Leu Glu Pro Trp Ile Ala Asn Asn Lys Asn Ala Tyr . 545 550 560
- Val Asp His Thr Gly Gly Ile Asn Gly Thr Lys Val Leu Tyr Val His 565 570 575

Lys Asp Gly Glu Phe Ser Gln Phe Val Gly Gly Lys Leu Lys Ser Lys 580 585 590

Thr Glu Tyr Val Ile Gln Tyr Ile Val Lys Gly Lys Ala Ser Ile Tyr 595 600 605

Leu Lys Asp Lys Lys Asn Glu Asn Ser Ile Tyr Glu Glu Ile Asn Asn 610 615 620

Asp Leu Glu Gly Phe Gln Thr Val Thr Lys Arg Phe Ile Thr Gly Thr 625 630 635 640

Asp Ser Ser Gly Ile His Leu Ile Phe Thr Ser Gln Asn Gly Glu Gly
645 650 655

Ala Phe Gly Gly Asn Phe Ile Ile Ser Glu Ile Arg Thr Ser Glu Glu
660 665 670

Leu Leu Ser Pro Glu Leu Ile Met Ser Asp Ala Trp Val Gly Ser Gln 675 680 685

Gly Thr Trp Ile Ser Gly Asn Ser Leu Thr Ile Asn Ser Asn Val Asn 690 695 700

Gly Thr Phe Arg Gln Asn Leu Pro Leu Glu Ser Tyr Ser Thr Tyr Ser 705 710 715 720

Met Asn Phe Thr Val Asn Gly Phe Gly Lys Val Thr Val Arg Asn Ser 725 730 735

Arg Glu Val Leu Phe Glu Lys Ser Tyr Pro Gln Leu Ser Pro Lys Asp 740 745 750

Ile Ser Glu Lys Phe Thr Thr Ala Ala Asn Asn Thr Gly Leu Tyr Val 755 760 765

Glu Leu Ser Arg Ser Thr Ser Gly Gly Ala Ile Asn Phe Arg Asp Phe 770 780

Ser Ile Lys 785

<210> 26

<211> 2367

<212> DNA

<213> Bacillus thuringiensis

<400> 26

atggctaaca tgaacaacac caagctcaac gcccgcgccc tcccatcctt cattgactac 60 ttcaacggca tctacggctt cgccactggc atcaaggaca tcatgaacat gatcttcaag 120 actgacactg gtggcaacct caccttggat gagatcctca agaaccagca gctcctcaac 180 gagatetetg geaagttgga tggtgteaac ggeteeetea acgaeeteat tgeeeaggge 240 aacctcaaca ctgagctttc caaggagatc ctcaaaattg ccaacgagca gaaccaggtc 300 ctcaacgatg tcaacaacaa gttggatgcc atcaacacca tgctccacat ctatctccca 360 aaaatcacct ccatgetete tgatgteatg aageagaact aegeeetete cetecaagtg 420 gagtacetet ccaagcaget caaggaaatt tetgacaagt tggatgtgat caacgteaac 480 gtecteatea actecaceet caetgagate actecageet ateagaggat caagtacgte 540 aacgagaagt tcgaggagct tactttcgcc actgagacca ccctcaaggt caagaaggac 600 tecageceag etgaeatett ggatgagett aetgagetta etgagttgge eaagtetgte 660 accaagaacg atgtggatgg cttcgagttc tacctcaaca ccttccacga tgtcatggtg 720 ggcaacaact tgttcggccg ttctgccctc aagactgcct ctgaattgat cgcaaaggag 780 aacgtcaaga cctctggctc tgaggtgggc aacgtctaca acttcctcat tgtcctcact 840 gccctccaag ccaaggcett cctcacecte accacetgte gtaagetett gggettgget 900 gacattgact acacetecat catgaacgag caceteaaca aggagaagga ggagtteegt 960 1020 gtcaacatcc tcccaaccct ctccaacacc ttctccaacc caaactacgc caaggtcaag 1080 ggctctgatg aggatgccaa gatgattgtg gaggccaagc ccggccacgc ccttgtgggc 1140 ttcgagatet ccaacgacte catgactgte etcaaggtet acgaggecaa geteaageag 1200 aactaccagg tggacaagga ctccctctcc gaggtcatct actccgacat ggacaagctc 1260 ctctgcccag accagtccga gcagatctac tacaccaaca acatcgtgtt cccaaacgag 1320 tacgtcatca ccaaaattga cttcaccaag aagatgaaaa ccctccgtta cgaggtcact 1380 gccaactcct acgactcctc cactggtgag attgacctca acaagaagaa ggtggagtcc totgaggotg agtacogtac cotototgoc aacaacgatg gtgtotacat gooottgggt 1440 gtgatetetg agacetteet cacteetate aacggttteg geetecaage tgatgaaaat 1500 teaegtetea teaeceteae tigtaagtee tateteaggg agtigetett ggecaetgae 1560

T:\Sequences\Mycogen\MA-708CDC1\MA-708CDC1.ST25.txt/DNB/ehm

ctctccaaca	aggagaccaa	gctcattgtc	ccacccatct	ccttcatctc	caacattgtg	1620
gagaacggca	acttggaggg	tgagaacttg	gagccttgga	ttgccaacaa	caagaacgcc	1680
tacgtggacc	acactggtgg	catcaacggc	accaaggtcc	tctacgtcca	caaggatggt	1740
gagttctccc	agttcgtggg	tggcaagttg	aagtccaaga	ctgagtacgt	catccagtac	1800
attgtcaagg	gcaaggcctc	catctatctc	aaggacaaga	aaaatgagaa	ctccatctac	1860
gaggagatca	acaacgactt	ggagggette	cagactgtca	ccaagaggtt	catcactggc	1920
actgactcct	ctggcatcca	cctcatcttc	acctcccaga	acggtgaggg	tgctttcggt	1980
ggcaacttca	taatctctga	gatcaggacc	tctgaggagc	ttctctctcc	cgagcttatc	2040
atgtctgatg	cctgggttgg	ctcccagggc	acttggatct	ctggcaactc	cctcaccatc	2100
aactccaacg	tcaacggcac	cttccgccag	aacctcccat	tggagtccta	ctccacctac	2160
tccatgaact	tcactgtcaa	cggtttcggc	aaggtcactg	tcaggaactc	ccgtgaggtc	2220
ctcttcgaga	agtcctaccc	acagetetet	cccaaggaca	tctctgagaa	gttcaccact	2280
gctgccaaca	acactggcct	ctacgtggag	ctttcccgtt	ccacctctgg	tggtgccatc	2340
aacttccgtg	acttctccat	caagtga			•	2367

<210> 27

<211> 788

<212> PRT

<213> Bacillus thuringiensis

<400> 27

Met Ala Asn Met Asn Asn Thr Lys Leu Asn Ala Arg Ala Leu Pro Ser 1 5 10 15

Phe Ile Asp Tyr Phe Asn Gly Ile Tyr Gly Phe Ala Thr Gly Ile Lys 20 25 30

Asp Ile Met Asn Met Ile Phe Lys Thr Asp Thr Gly Gly Asn Leu Thr 35 40 45

Leu Asp Glu Ile Leu Lys Asn Gln Gln Leu Leu Asn Glu Ile Ser Gly 50 55 60

Lys Leu Asp Gly Val Asn Gly Ser Leu Asn Asp Leu Ile Ala Gln Gly 65 70 75 80

Asn	Leu	Asn	Thr	Glu	Leu	Ser	Lys	Glu	Ile	Leu	Lys	Ile	Ala	Asn	Glu
				85					90					95	

Gln Asn Gln Val Leu Asn Asp Val Asn Asn Lys Leu Asp Ala Ile Asn 100 105 110

Thr Met Leu His Ile Tyr Leu Pro Lys Ile Thr Ser Met Leu Ser Asp 115 120 125

Val Met Lys Gln Asn Tyr Ala Leu Ser Leu Gln Val Glu Tyr Leu Ser 130 135 140

Val Leu Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln Arg 165 170 175

Ile Lys Tyr Val Asn Glu Lys Phe Glu Glu Leu Thr Phe Ala Thr Glu 180 185 190

Thr Thr Leu Lys Val Lys Lys Asp Ser Ser Pro Ala Asp Ile Leu Asp 195 200 205

Glu Leu Thr Glu Leu Thr Glu Leu Ala Lys Ser Val Thr Lys Asn Asp 210 215 220

Val Asp Gly Phe Glu Phe Tyr Leu Asn Thr Phe His Asp Val Met Val 225 230 235 240

Gly Asn Asn Leu Phe Gly Arg Ser Ala Leu Lys Thr Ala Ser Glu Leu 245 250 255

Ile Ala Lys Glu Asn Val Lys Thr Ser Gly Ser Glu Val Gly Asn Val
260 265 270

Tyr Asn Phe Leu Ile Val Leu Thr Ala Leu Gln Ala Lys Ala Phe Leu 275 280 285

Thr Leu Thr Thr Cys Arg Lys Leu Leu Gly Leu Ala Asp Ile Asp Tyr 290 295 300

Thr Ser Ilè Met Asn Glu His Leu Asn Lys Glu Lys Glu Glu Phe Arg 305 310 315 320

Val Asn Ile Leu Pro Thr Leu Ser Asn Thr Phe Ser Asn Pro Asn Tyr 325 330 335

Ala Lys Val Lys Gly Ser Asp Glu Asp Ala Lys Met Ile Val Glu Ala 340 345 350

Lys Pro Gly His Ala Leu Val Gly Phe Glu Ile Ser Asn Asp Ser Met 355 360 365

Thr Val Leu Lys Val Tyr Glu Ala Lys Leu Lys Gln Asn Tyr Gln Val 370 375 380

Asp Lys Asp Ser Leu Ser Glu Val Ile Tyr Ser Asp Met Asp Lys Leu 385 390 395 400

Leu Cys Pro Asp Gln Ser Glu Gln Ile Tyr Tyr Thr Asn Asn Ile Val405 410 415

Phe Pro Asn Glu Tyr Val Ile Thr Lys Ile Asp Phe Thr Lys Lys Met 420 425 430

Lys Thr Leu Arg Tyr Glu Val Thr Ala Asn Ser Tyr Asp Ser Ser Thr 435 440 445

Gly Glu Ile Asp Leu Asn Lys Lys Lys Val Glu Ser Ser Glu Ala Glu
450 455 460

Tyr Arg Thr Leu Ser Ala Asn Asn Asp Gly Val Tyr Met Pro Leu Gly 465 470 475 480

Val Ile Ser Glu Thr Phe Leu Thr Pro Ile Asn Gly Phe Gly Leu Gln 485 490 495

Ala Asp Glu Asn Ser Arg Leu Ile Thr Leu Thr Cys Lys Ser Tyr Leu
500 505 510

Arg Glu Leu Leu Leu Ala Thr Asp Leu Ser Asn Lys Glu Thr Lys Leu 515 520 525

Ile Val Pro	Pro Ile	Ser	Phe	Ile	Ser	Asn	Ile	Val	Glu	Asn	Gly	Asn
530			535					540				

Leu Glu Gly Glu Asn Leu Glu Pro Trp Ile Ala Asn Asn Lys Asn Ala 545 550 555 560

Tyr Val Asp His Thr Gly Gly Ile Asn Gly Thr Lys Val Leu Tyr Val 565 570 575

His Lys Asp Gly Glu Phe Ser Gln Phe Val Gly Gly Lys Leu Lys Ser 580 585 590

Lys Thr Glu Tyr Val Ile Gln Tyr Ile Val Lys Gly Lys Ala Ser Ile 595 600 605

Tyr Leu Lys Asp Lys Lys Asn Glu Asn Ser Ile Tyr Glu Glu Ile Asn 610 620

Asn Asp Leu Glu Gly Phe Gln Thr Val Thr Lys Arg Phe Ile Thr Gly 625 630 635 640

Thr Asp Ser Ser Gly Ile His Leu Ile Phe Thr Ser Gln Asn Gly Glu 645 650 655

Gly Ala Phe Gly Gly Asn Phe Ile Ile Ser Glu Ile Arg Thr Ser Glu 660 665 670

Glu Leu Leu Ser Pro Glu Leu Ile Met Ser Asp Ala Trp Val Gly Ser 675 680 685

Gln Gly Thr Trp Ile Ser Gly Asn Ser Leu Thr Ile Asn Ser Asn Val 690 695 700

Asn Gly Thr Phe Arg Gln Asn Leu Pro Leu Glu Ser Tyr Ser Thr Tyr 705 710 715 720

Ser Met Asn Phe Thr Val Asn Gly Phe Gly Lys Val Thr Val Arg Asn 725 730 735

Ser Arg Glu Val Leu Phe Glu Lys Ser Tyr Pro Gln Leu Ser Pro Lys 740 745 750 Asp Ile Ser Glu Lys Phe Thr Thr Ala Ala Asn Asn Thr Gly Leu Tyr 755 760 765

Val Glu Leu Ser Arg Ser Thr Ser Gly Gly Ala Ile Asn Phe Arg Asp 770 775 780

Phe Ser Ile Lys 785